FIG. 2b is the nucleotide sequence of GFP (SEQ ID NO: 21);

FIG. 3 is the DNA (SEQ ID NO: 15) and predicted amino acid sequence (SEQ ID NO: 16) and predicted amino acid sequence of (SEQ ID NO: 16) of F64L-Y66H-GFP;

FIG. 4 is the DNA (SEQ ID NO: 17) and predicted amino acid sequence (SEQ ID NO: 18) of F64L-GFP;

FIG. 5 is the DNA (SEQ ID NO: 19) and predicted amino acid sequence (SEQ ID NO: 20) of F64L-S65T-GFP;

FIG. 6a is a graph of fluorescence emission spectra measured in cells grown at 22°C for 16 hours and excited with light at 398 nm for F64L-GFP, GFP, GFP-N1, F64L-S65T-GFP, and lacZ;

FIG. 6b is a graph of fluorescence emission spectra measured in cells grown at 37°C for 16 hours and excited with light at 398 nm for F64L-GFP, GFP, GFP-N1, F64L-S65T-GFP, and lacZ;

FIG. 6c is a graph of fluorescence emission spectra measured in cells grown at 22°C for 16 hours and excited with light at 470 nm for F64L-GFP, GFP, GFP-N1, F64L-S65T-GFP, and lacZ;

FIG. 6d is a graph of fluorescence emission spectra measured in cells grown at 37°C for 16 hours and excited with light at 470 nm for F64L-GFP, GFP, GFP-N 1, F64L-S65T-GFP, and lacZ;

FIG. 6e is a graph of fluorescence emission spectra measured in cells grown at 22°C for 16 hours and excited with light at 380 nm for F64L-Y66H-GFP, Y66H-GFP and lacZ;

FIG. 6f is a graph of fluorescence emission spectra measured in cells grown at 37°C for 16 hours and excited with light at 380 nm for F64L-Y66H-GFP, Y66H-GFP and lacZ.--

Please replace the paragraph beginning on page 12, line 25, with the following rewritten paragraph:

--Briefly, total RNA, isolated from A. victoria by a standard procedure (Sambrook et al., Molecular Cloning. 2., eds. (1989) (Cold Spring Harbor Laboratory Press: Cold Spring Harbor, N.Y.), 7.19-7.22) was converted into cDNA by using the AMV reverse transcriptase (Promega, Madison, Wis., USA) as recommended by the manufacturer. The cDNA was then PCR amplified, using PCR primers designed on the basis of a previously published GFP sequence (Prasher et al., Gene 111 (1992), 229-233; GenBank accession No. M62653) together with the UlTma™ polymerase (Perkin Elmer, Foster City, CA, USA). The sequences of the primers were: GFP-2 (SEQ ID NO: 1): TGGAATAAGCTTTATGAGTAAAGGAGAAGAACTTTT and GFP-1 (SEQ ID NO:2): AAGAATTCGGATCCCTTTAGTGTCAATTGGAAGTCT--

Please replace the paragraph beginning on page 12, line 34, with the following rewritten paragraph:

--Restriction endonuclease sites inserted in the 5' (a HindIII site) and 3' (EcoRI and BamHI sites) primers facilitated the cloning of the PCR amplified GFP cDNA into a slightly modified pUC19 vector. The details of the

construction are as follows: LacZ Shine-Dalgarno AGGA, immediately followed by the 5' HindIII site plus an extra T and the GFP ATG codon, giving the following DNA sequence (SEQ ID NO: 23) at the lacZ-promoter GFP fusion point: P_{LacZ} - AGGAAAGCTTTATG-*GFP*. At the 3' end of the GFP cDNA, the base pair corresponding to nucleotide 770 in the published GFP sequence (GenBank accession No. M62653) was fused to the EcoR1 site of the pUC19 multiple cloning site (MCS) through a PCR generated BamHI, EcoRI linker region).--

Please delete pages 20-23 of the specification containing the Sequence Listing. Please renumber the remaining pages of the specification, beginning with the claims, consecutively from page 20. Please insert the Substitute Sequence Listing enclosed herewith immediately after the abstract.

In the Figures

Please replace Figures 2a, 3, 4, and 5 with the substitute drawings enclosed herewith.